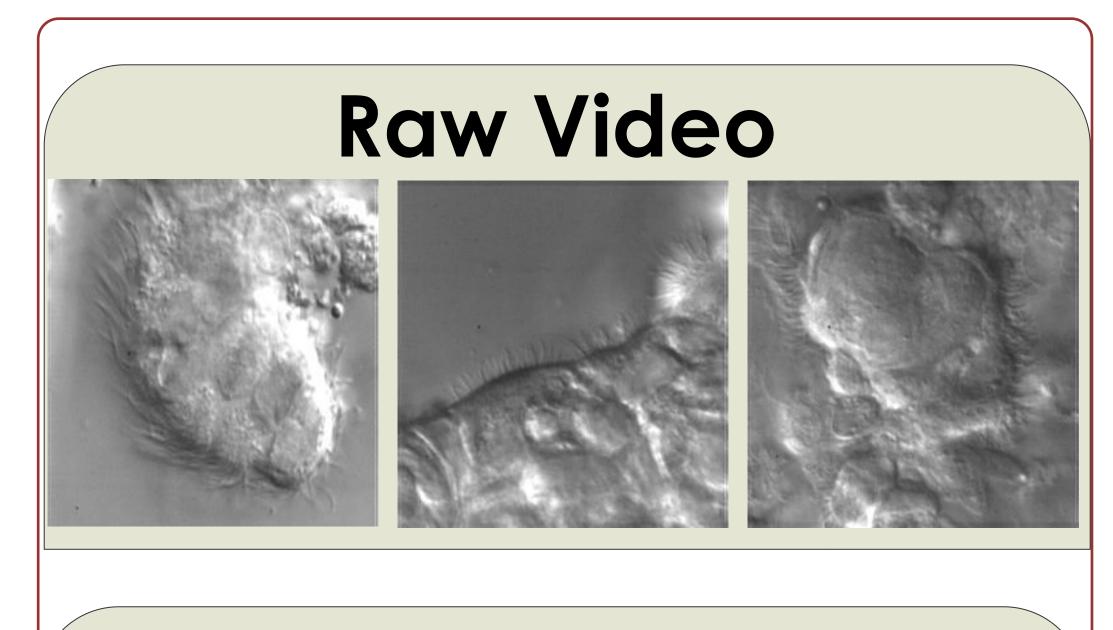
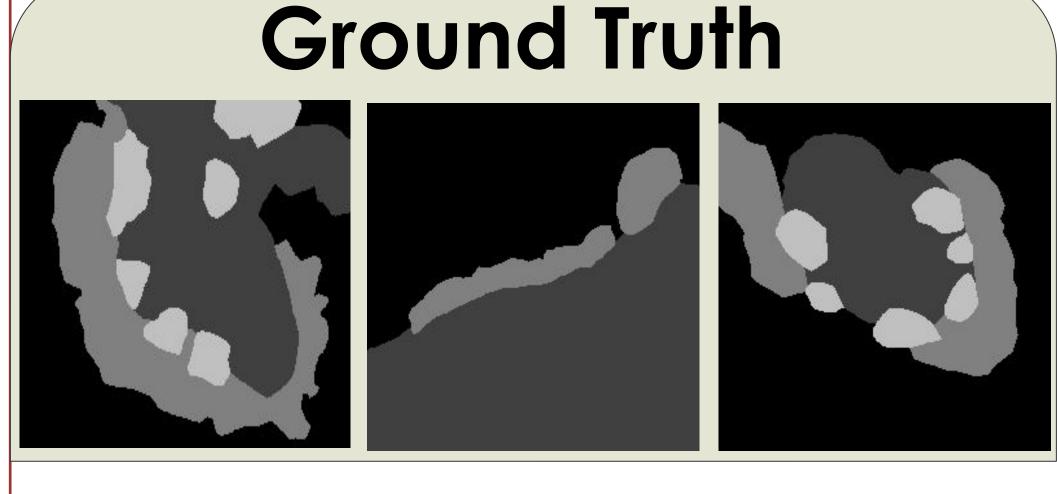
Stacked Neural Networks for Automated https://quinngroup.github.io Ciliary Motion Analysis

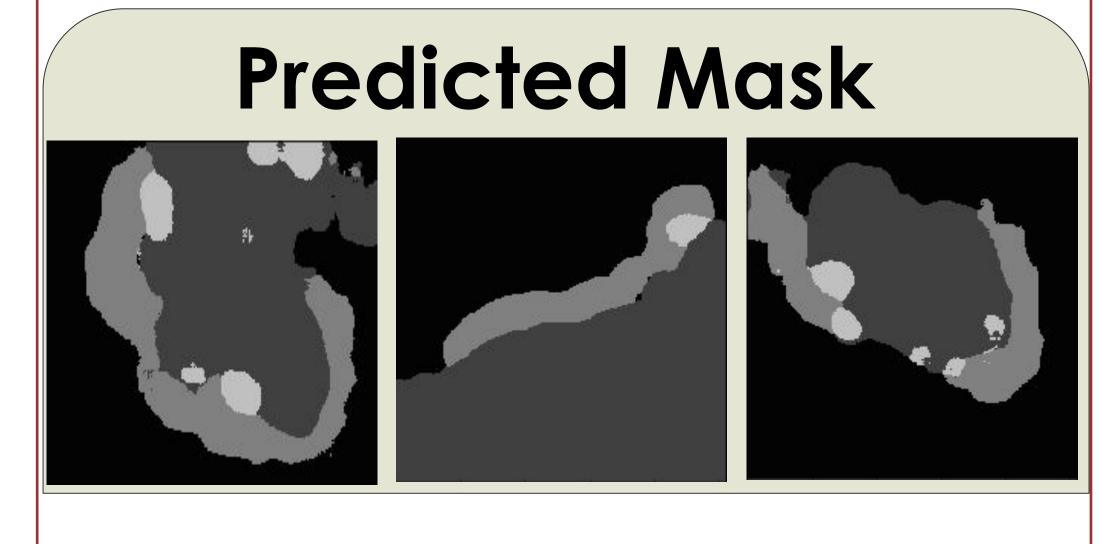
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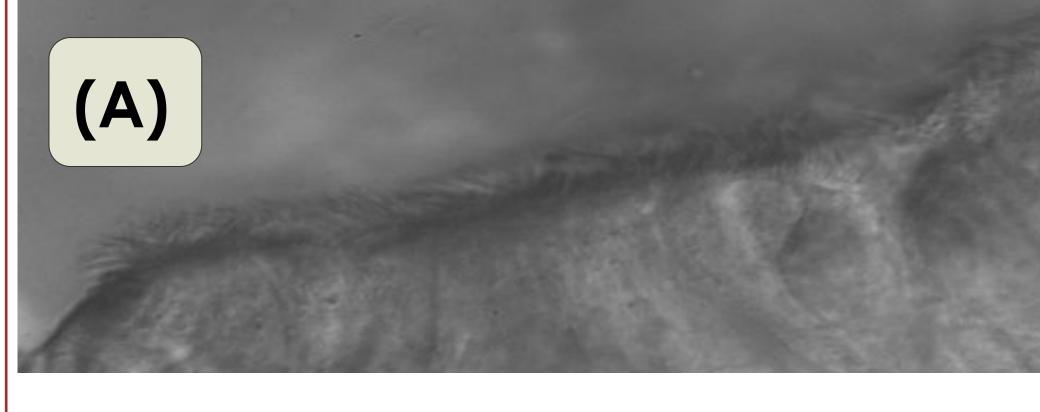
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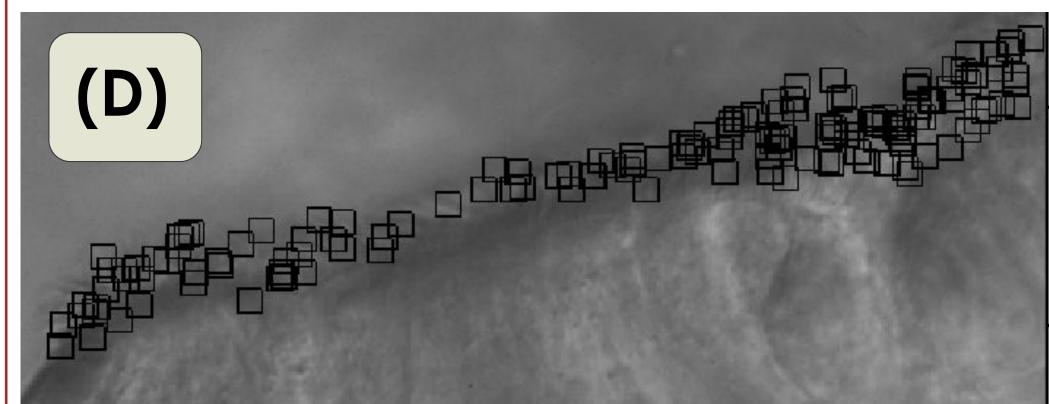


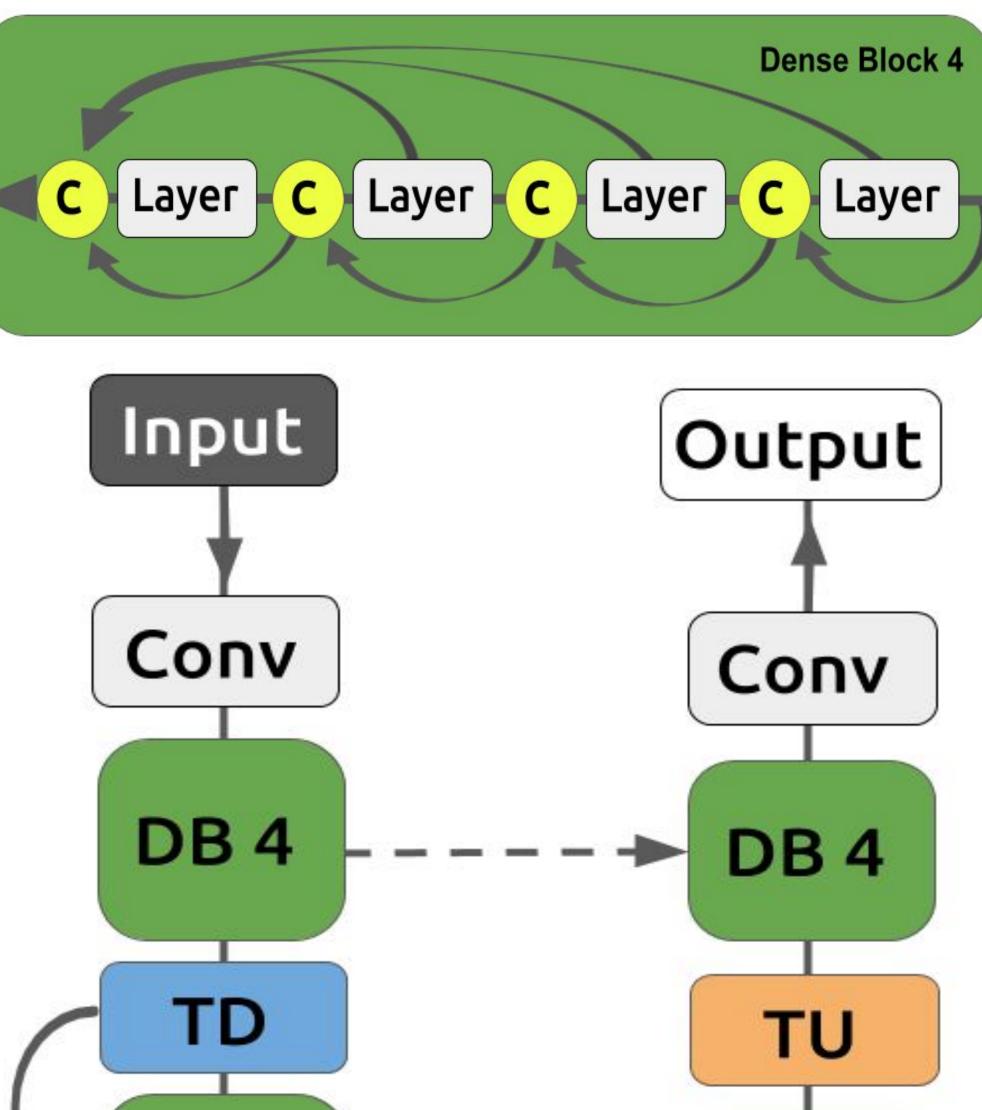


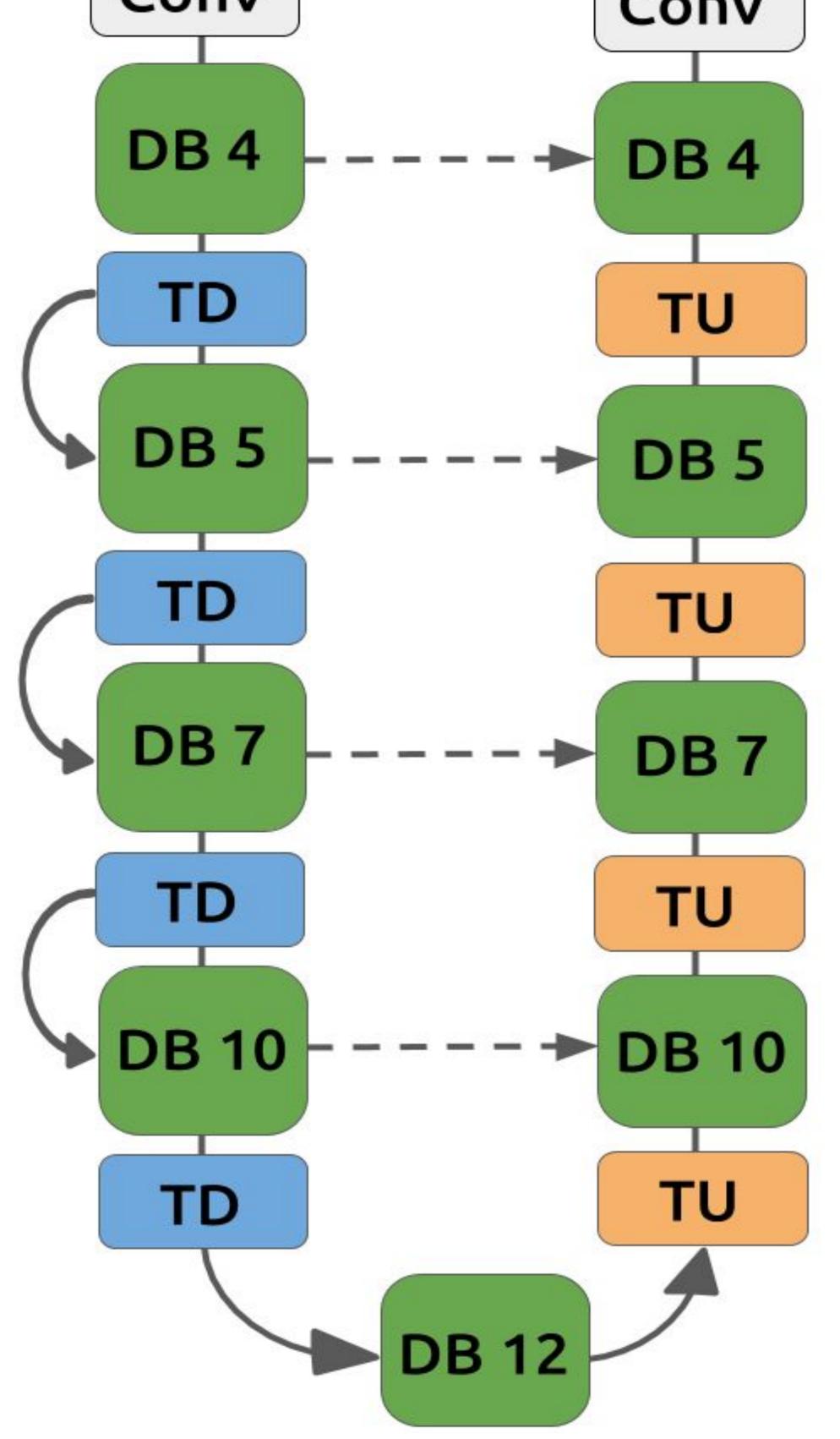












Transition Up **Transition Down Batch Normalization Batch Normalization** ReLU Activation ReLU Activation 3 x 3 Transposed 1 x 1 Convolution Stride 2 Convolution Stride 2

What are Cilia?

- Cilia are hairlike structures found on nearly every cell in the body and are responsible for regulating the respiratory system and nutrient delivery.
- Diseases known as ciliopathies, where ciliary motion becomes abnormal, can result in a wide spectrum of disorders such as sinopulmonary disease, congenital heart disease, and birth defects.

The Problem

- Current techniques for assessing ciliary motion rely on manual segmentation of cilia, which is time consuming, error-prone, and does not scale well.
- Another issue is the lack of consensus in classifying different types of ciliary motion even among experts from different clinicians.
- Cilia segmentation is challenging due to their small, hair-like shape, in addition to varying camera artifacts, orientation, and lighting.

The Data

- Our data consisted of nasal brush biopsies from 75 patients (35 healthy controls, 40 with a diagnosed ciliopathy), totaling 268 microscopy videos.
- To establish ground truth, these videos were analyzed by a blind panel of researchers labeling abnormal motion with a majority vote.

<u>Preprocessing</u>

- To reduce variance of different lighting and perspective orientations, we computed optical flow over the video to derive differential invariants: rotation, divergence and deformation.
- We only consider rotation for motion classification.

Cilia Segmentation

- The first neural network in our pipeline is a fully convolutional DenseNet (74 layers) which segments regions of cilia from surrounding cell bodies.
- We train this network to semantically segment four classes: cell body, side cilia, top cilia, and background but only a binary mask of cilia (B).
- After obtaining predicted segmentation maps, we compute a simple probability map using mean distance metric (C) and randomly sample patches from this distribution (D).

Motion Classification

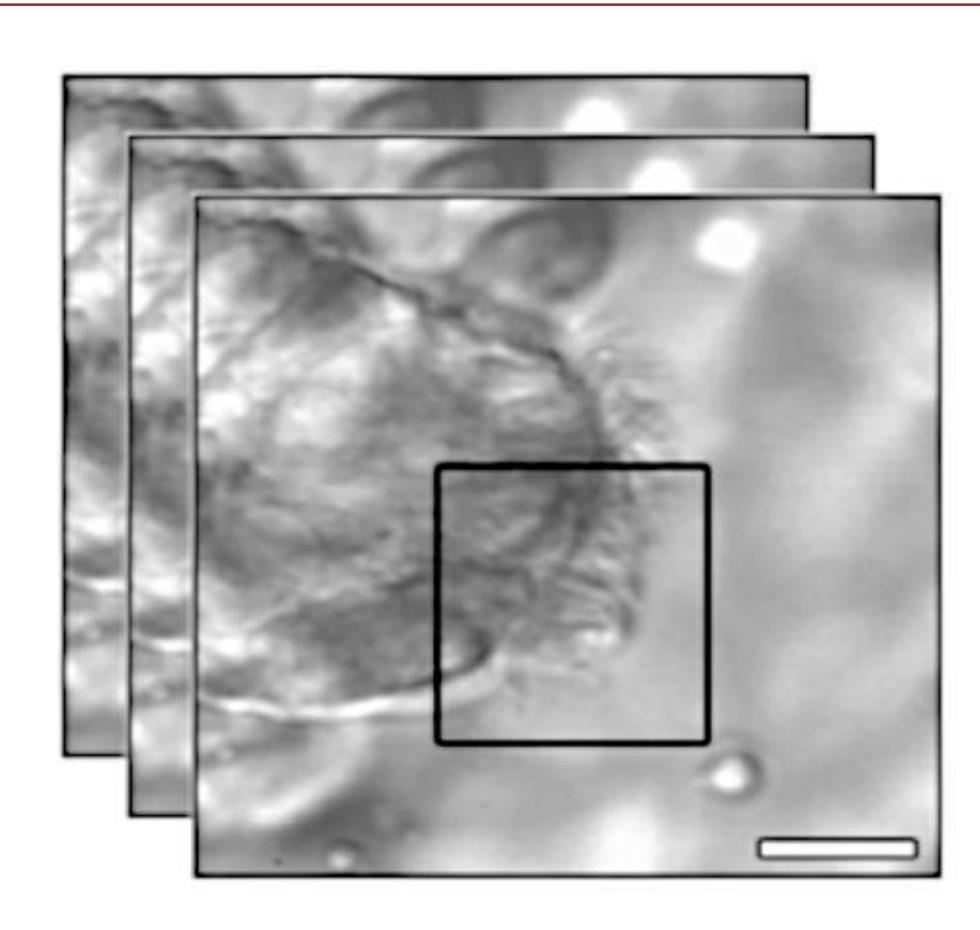
- The second neural network in our pipeline is is a Convolutional Long Short Term Memory (LSTM) networks, which take into account both spatial and temporal dependencies.
- Convolutional LSTM are like regular LSTM but the inputs to each gate inside a LSTM cell are convolved to extract spatial features.

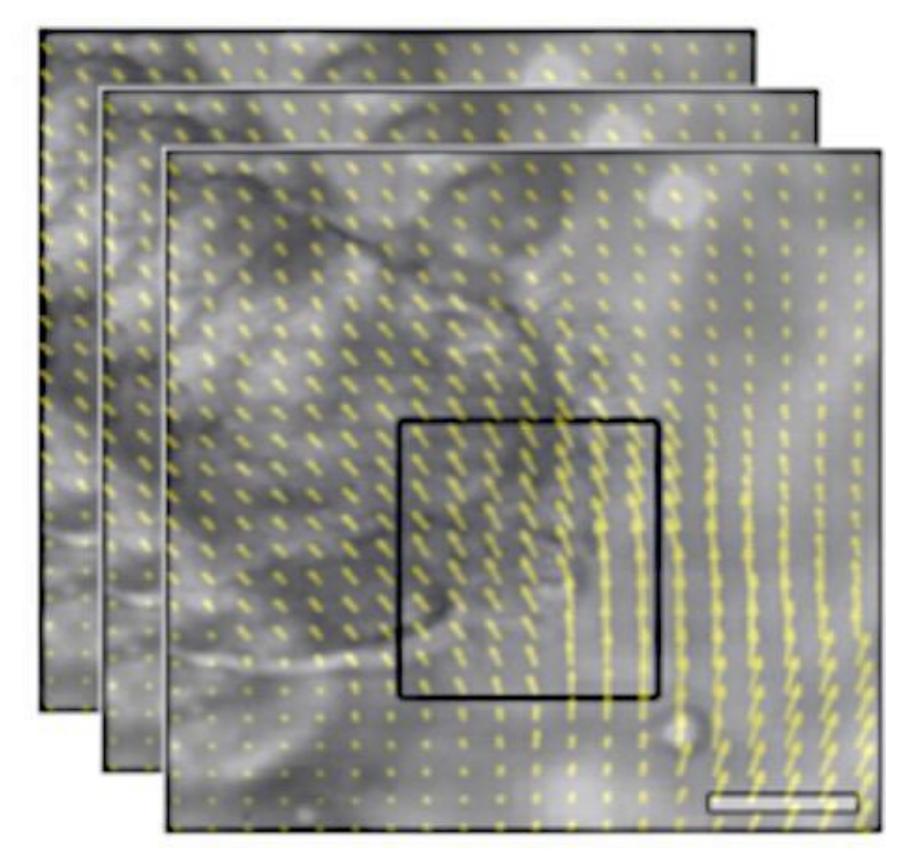
DenseNets

- DenseNet are composed of Denseblocks (DB), Transition Down (TD) blocks, and Transition Up (TU) blocks.
- Whereas Resnets use a summation and an identity mapping, DenseNets use concatenation to maximize feature reuse between all layers in a Dense Block.
- DenseNets excel in feature efficiency and have an inherently regularizing property, especially suitable for small datasets.

Future Work

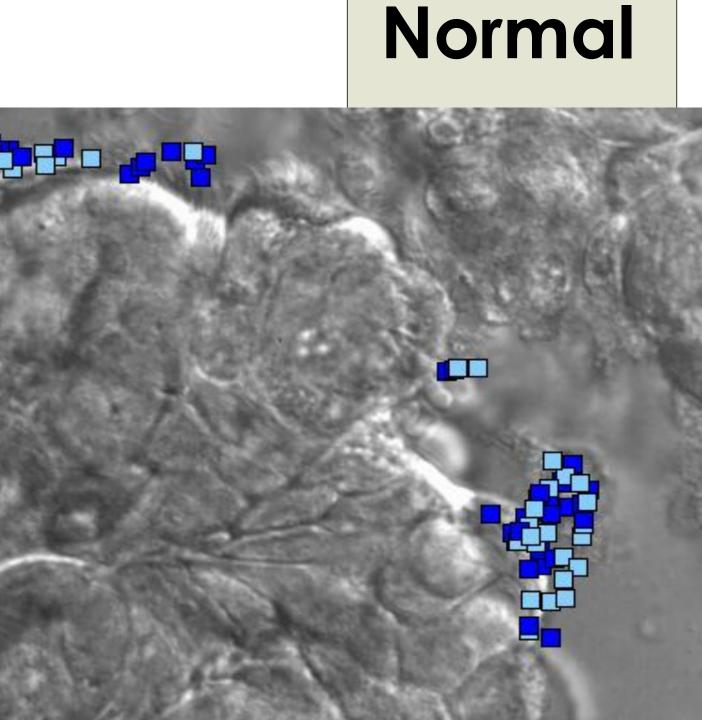
- Unsupervised segmentation of cilia
- Generative Adversarial Networks (GAN) to model different kinds of ciliary motion
- Conditional Random Fields (CRF) post-processing for finer segmentation maps

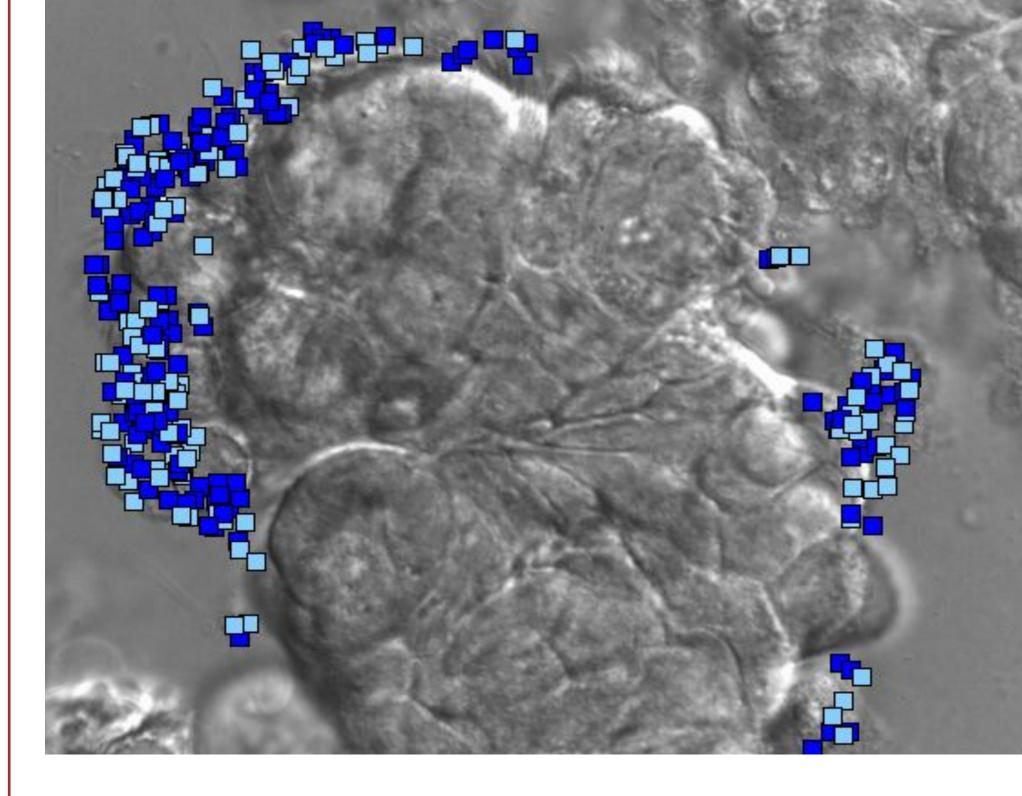


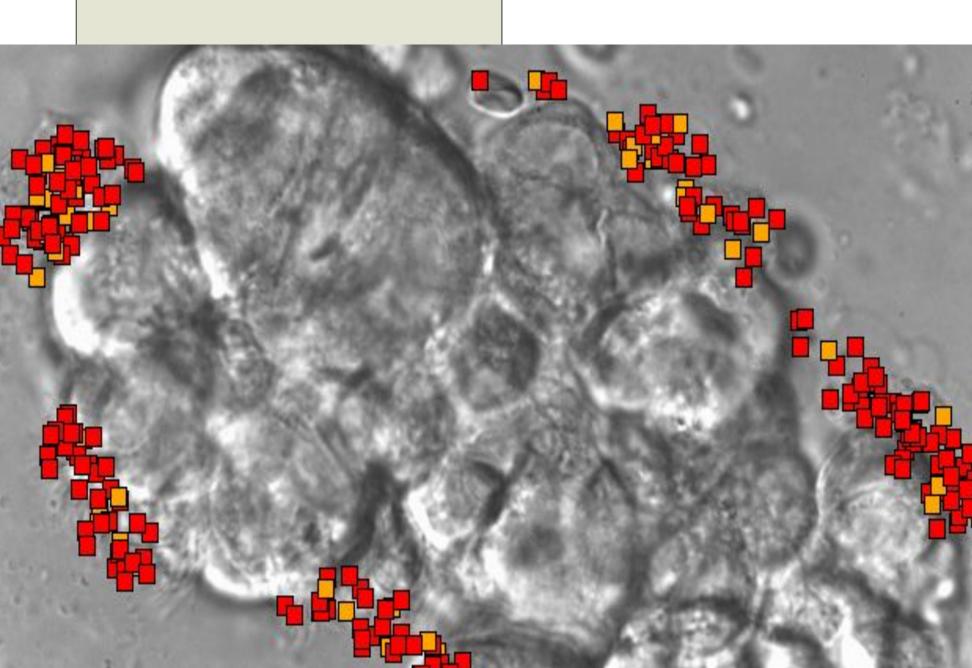


Convolutional LSTM

 $f_t = \sigma(W_f * x_t + U_f * h_{t-1} + V_f \circ c_{t-1} + b_f)$ $i_t = \sigma(W_i * x_t + U_i * h_{t-1} + V_i \circ c_{t-1} + b_i)$ $o_t = \sigma(W_o * x_t + U_o * h_{t-1} + V_o \circ c_{t-1} + b_o)$ $c_t = f_t \circ c_{t-1} + i_t \circ \sigma(W_c * x_t + U_c * h_{t-1} + b_c)$ $h_t = o_t \circ \sigma_h(c_t)$







Abnormal

	Normal (predicted)		
Normal (actual)	27		
Abnormal (actual)	1		

Normal (actual)	8
Abnormal (actual)	39

Abnormal (predicted)

Epochs	Accuracy	F1	Recall	Precision
100	0.81	0.84	0.93	0.77
200	0.88	0.90	0.98	0.83

References

Simon Je gou, Michal Drozdzal, David Vazquez, Adriana Romero, and Yoshua Bengio, "The one hundred layers tiramisu: Fully convolutional densenets for semantic segmen- tation," in Computer Vision and Pattern Recognition Work- shops (CVPRW), 2017 IEEE Conference on. IEEE, 2017, pp. 1175–1183.

S. Quinn, M. Zahid, J. Durkin, R. Francis, C. W. Lo, and C. Chennubhotla. "Automated identification of abnormal respiratory ciliary motion in nasal biopsies." Science Translational Medicine.

S. Quinn, R. Francis, C. W. Lo, and C. Chennubhotla. "Novel Use of Differential Image Velocity Invariants to Categorize Ciliary Motion Defects." Proceedings in the Biomedical Science and Engineering Conference.